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۹	April 2001 Proceedings of the fifth annual international conference on Computational biology	
•	Publisher: ACM Press	
	Full text available: pdf(623.73 KB) Additional Information: full citation, abstract, references, index terms	
	High-throughput, data-directed computational protocols for <i>Structural Genomics</i> (or <i>Proteomics</i> ) are required in order to evaluate the protein products of genes for structure and function at rates comparable to current gene-sequencing technology. To develop such methods, new algorithms are required that can quickly extract significantly more structural information from sparse experimental data. This paper presents a new class of signal processing algorithms for nuclear magnetic re	
4	A NMR-spectra-based scoring function for protein docking	_
_	O. Kohlbacher, A. Burchardt, A. Moll, A. Hildebrandt, P. Bayer, HP Lenhof	-
<b>③</b>	April 2001 Proceedings of the fifth annual international conference on Computational	
	biology Bublisham ACM Press	
	Publisher: ACM Press Full text available: pdf(262.27 KB) Additional Information: full citation, abstract, references, index terms	
	A well studied problem in the area of Computational Molecular Biology is the so-called Protein-Protein Docking problem (PPD) that can be formulated as follows: Given two proteins A and B that form a protein complex, compute the 3D-structure of the protein complex AB. Protein docking algorithms can be used to study the driving forces and reaction mechanisms of docking processes. They are also able to speed up the lenghty process of experimental structure elucidation of pro	
5	Level set and PDE methods for computer graphics	_
<b>②</b>	David Breen, Ron Fedkiw, Ken Museth, Stanley Osher, Guillermo Sapiro, Ross Whitaker August 2004 Proceedings of the conference on SIGGRAPH 2004 course notes GRAPH '04	
	Publisher: ACM Press	
	Full text available: pdf(17.07 MB) Additional Information: full citation, abstract	
	Level set methods, an important class of partial differential equation (PDE) methods, define dynamic surfaces implicitly as the level set (iso-surface) of a sampled, evolving nD function. The course begins with preparatory material that introduces the concept of using partial differential equations to solve problems in computer graphics, geometric modeling and computer vision. This will include the structure and behavior of several different types of differential equations, e.g. the level set eq	
6	Matching simulation and experiment (extended abstract): a new simplified model for	_
٩	and the control of th	
~	Jon M. Sorenson, Teresa Head-Gordon	
	April 2000 Proceedings of the fourth annual international conference on	
	Computational molecular biology Publisher: ACM Press	
	Full text available: pdf(951.54 KB) Additional Information: full citation, abstract, references	

Simulations of simplified protein folding models have provided much insight into solving the protein folding problem. We propose here a new off-lattice bead model, capable of simulating several different fold classes of small proteins. We present the sequence for an &agr;/&bgr; protein resembling the IgG-binding proteins L and G. The thermodynamics of the folding process for this model are characterized using the multiple multi-histogram method combined with constant-temperature Langevin simu ...

ARGOS: An operating system for a computer utility supporting interactive instrument control

<b>\rightarrow</b>	Paul Day, John Hines January 1973 ACM SIGOPS Operating Systems Review, Proceedings of the fourth ACM symposium on Operating system principles SOSP '73, Volume 7 Issue 4 Publisher: ACM Press Full text available: pdf(750.58 KB) Additional Information: full citation, abstract, references, index terms							
	"ARGOS" (ARGonne Operating System), which runs on a Xerox Sigma 5 hardware configuration, provides a dynamic multiprogrammed environment which supports the following: data acquisition and interactive control for numerous (currently 19) independently running on-line laboratory experiments; three interactive graphics terminals; FORTRAN IV-H executing at each of 23 remote time-shared terminals; a jobstream from open-shop batch processing; long-term low priority computations (100 CP							
8	Efficient database screening for rational drug design using pharmacophore-							
<b>\rightarrow</b>	constrained conformational search Steven M. LaValle, Paul W. Finn, Lydia E. Kavraki, Jeal-Claude Latombe April 1999 Proceedings of the third annual international conference on Computational molecular biology Publisher: ACM Press							
	Full text available: pdf(1.70 MB)  Additional Information: full citation, references, citings, index terms							
9	Probabilistic models of indexing and searching							
	S. E. Robertson, C. J. van Rijsbergen, M. F. Porter June 1980 Proceedings of the 3rd annual ACM conference on Research and development in information retrieval							
	Publisher: Butterworth & Co.  Full text available: pdf(907.71 KB) Additional Information: full citation, references, citings							
10	Visualization: A toolkit for visualizing biomedical data sets							
<b>③</b>	Burkhard C. Wünsche February 2003 Proceedings of the 1st international conference on Computer graphics							
	and interactive techniques in Australasia and South East Asia Publisher: ACM Press							
	Full text available: pdf(2.33 MB)  Additional Information: full citation, abstract, references, citings, index terms							
	Medical data sets now comprise a diverse range of measurements such as tissue densities, sensitivity to magnetization, blood flow velocity, and material strain. The size and complexity of medical data sets makes it increasingly difficult to understand, compare, analyze and communicate the data. Visualization is an attempt to simplify these tasks according to the motto "An image says more than a thousand words". Representing complex material properties, such as strain, as a single image improves							
	<b>Keywords</b> : biomedicine, tensor fields, user interfaces, visualization							
11 <b>③</b>	January 1969 Proceedings of the third conference on Hypercube concurrent							
	computers and applications - Volume 2 Publisher: ACM Press							
	Full text available:  Additional Information: <u>full citation</u> , <u>abstract</u> , <u>references</u> , <u>citings</u> , <u>index</u>							

pdf(4.08 MB)

terms.

We briefly review some key scientific and parallel processing issues in a selection of some 84 existing applications of parallel machines. We include the MIMD hypercube transputer array, BBN Butterfly, and the SIMD ICL DAP, Goodyear MPP and Connection Machine from Thinking Machines. We use a space-time analogy to classify problems and show how a division into synchronous, loosely synchronous and asynchronous problems is helpful. This classifies problems into those suitable for SIMD or MIMD ...

12 Event choice datalog: a logic programming language for reasoning in multiple

dimensions

Gianluigi Greco, Antonella Guzzo, Domenico Saccà, Francesco Scarcello August 2004 Proceedings of the 6th ACM SIGPLAN international conference on Principles and practice of declarative programming

Publisher: ACM Press

Full text available: Additional Information: full citation, abstract, references, index terms

This paper presents a rule-based declarative database language which extends DATALOG to express events and nondeterministic state transitions, by using the choice construct to model uncertainty in dynamic rules. The proposed language, called Event Choice DATALOG (DATALOG<sup>lev</sup> for short), provides a powerful mechanism to formulate queries on the evolution of a knowledge base, given a sequence of events envisioned to occur in the future. A distinguished feature of this language is the use ...

Keywords: knowledge representation, logic programming

13 Large a polynomial-time nuclear vector replacement algorithm for automated NMR

resonance assignments

Christopher James Langmead, Anthony Yan, Ryan Lilien, Lincong Wang, Bruce Randall Donald

April 2003 Proceedings of the seventh annual international conference on Research in computational molecular biology RECOMB '03

Publisher: ACM Press

Full text available: pdf(2.14 MB)

Additional Information: full citation, abstract, references, citings, index terms

High-throughput NMR structural biology can play an important role in structural genomics. We report an automated procedure for high-throughput NMR resonance assignment for a protein of known structure, or of an homologous structure. These assignments are a prerequisite for probing protein-protein interactions, protein-ligand binding, and dynamics by NMR. Assignments are also the starting point for structure determination and refinement. A new algorithm, called Nuclear Vector Replacement (NVR) ...

14 Pattern Mining: Multi-dimensional sequential pattern mining

Helen Pinto, Jiawei Han, Jian Pei, Ke Wang, Qiming Chen, Umeshwar Dayal

October 2001 Proceedings of the tenth international conference on Information and knowledge management

Publisher: ACM Press

Full text available: pdf(1.41 MB)

Additional Information: full citation, abstract, references, citings, index

Sequential pattern mining, which finds the set of frequent subsequences in sequence databases, is an important data-mining task and has broad applications. Usually, sequence patterns are associated with different circumstances, and such circumstances form a multiple dimensional space. For example, customer purchase sequences are associated with region, time, customer group, and others. It is interesting and useful to mine sequential patterns associated with multi-dimensional information. In this ...

15	Protein structure determination using protein threading and sparse NMR data						
<b>③</b>	(extended abstract)						
	Ying Xu, Dong Xu, Oakley H. Crawford, J. Ralph Einstein, Engin Serpersu April 2000 Proceedings of the fourth annual international conference on						
	Computational molecular biology						
	Publisher: ACM Press  Full text exclicit a publisher and tipes and						
	Full text available: pdf(663.42 KB) Additional Information: full citation, abstract, references, citings						
	It is well known that the NMR method for protein structure determination applies to small proteins and that its effectiveness decreases very rapidly as the molecular weight increases beyond about 30 kD. We have recently developed a method for protein structure determination that can fully utilize partial NMR data as calculation constraints. The core of the method is a threading algorithm that guarantees to find a globally optimal alignment between a query sequence and a template structure,						
	<b>Keywords</b> : NMR, energy minimization, fold recognition, protein structure determination, protein threading						
16 <b>③</b>	Multi-dimensional selectivity estimation using compressed histogram information  Ju-Hong Lee, Deok-Hwan Kim, Chin-Wan Chung  June 1999 ACM SIGMOD Record, Proceedings of the 1999 ACM SIGMOD international						
•	conference on Management of data SIGMOD '99, Volume 28 Issue 2						
	Publisher: ACM Press						
	Full text available: pdf(1.18 MB)  Additional Information: full citation, abstract, references, citings, index terms						
	The database query optimizer requires the estimation of the query selectivity to find the most efficient access plan. For queries referencing multiple attributes from the same relation, we need a multi-dimensional selectivity estimation technique when the attributes are dependent each other because the selectivity is determined by the joint data distribution of the attributes. Additionally, for multimedia databases, there are intrinsic requirements for the multi-dimensional selectivity esti						
17	An adaptive view element framework for multi-dimensional data management						
٩	John R. Smith, Chung-Sheng Li						
•	November 1999 Proceedings of the eighth international conference on Information and knowledge management						
	Publisher: ACM Press						
	Full text available: pdf(1.02 MB) Additional Information: full citation, abstract, references, index terms						
	We present an adaptive wavelet view element framework for managing different types of multi-dimensional data in storage and retrieval applications. We consider the problems of multi-dimensional data compression, multi-resolution subregion access, selective materialization, progressive retrieval and similarity searching. The framework uses wavelets to partition the multi-dimensional data into view elements that form the building blocks for synthesizing views of the data. The view ele						
	<b>Keywords</b> : OLAP, content-based search, data cubes, data management, digital libraries, information retrieval, multimedia database systems						
18	Multi-dimensional text classification						
	Thanaruk Theeramunkong, Verayuth Lertnattee August 2002 Proceedings of the 19th international conference on Computational linguistics - Volume 1	كحب					

Publisher: Association for Computational Linguistics

Co-Design

Full text available: 🔁 pdf(106.76 KB) Additional Information: full citation, abstract, references

This paper proposes a multi-dimensional framework for classifying text documents. In this framework, the concept of multidimensional category model is introduced for representing classes. In contrast with traditional flat and hierarchical category models; the multidimensional category model classifies each text document in a collection using multiple predefined sets of categories, where each set corresponds to a dimension. Since a multidimensional model can be converted to flat and hierarchica ...

19	On effective multi-dimensional indexing for strings	
٩	H. V. Jagadish, Nick Koudas, Divesh Srivastava	
•	May 2000 ACM SIGMOD Record, Proceedings of the 2000 ACM SIGMOD international conference on Management of data SIGMOD '00, Volume 29 Issue 2 Publisher: ACM Press	
	Full text available: pdf(1.15 MB)  Additional Information: full citation, abstract, references, citings, index terms	
	As databases have expanded in scope from storing purely business data to include XML documents, product catalogs, e-mail messages, and directory data, it has become increasingly important to search databases based on wild-card string matching: prefix matching, for example, is more common (and useful) than exact matching, for such data. In many cases, matches need to be on multiple attributes/dimensions, with correlations between the dimensions. Traditional multi-dimensional index structures,	
20	Fully Parallel Hardware/Software Codesign for Multi-Dimensional DSP Applications  Michael Sheliga, Nelson Luiz Passos, Edwin Hsing-Mean S' ha	

March 1996 Proceedings of the 4th International Workshop on Hardware/Software

Publisher: IEEE Computer Society Full text available: pdf(808.80 KB) Additional Information: full citation, abstract, citings

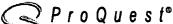
The design of multi-dimensional systems using hardware/software codesign allows a significant improvement in the development cycle. This paper presents a technique that enables a design to have arbitrarily high throughput by using multi-dimensional retiming techniques while adjusting the composition of hardware and multiple software elements in order to satisfy the area requirements. A multi-dimensional graph representing the problem is transformed and scheduled such that all nodes are executed ...

Keywords: Hardware/Software Codesign, Multi-Dimensional Systems, High Level Synthesis

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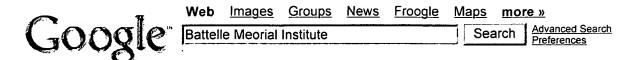
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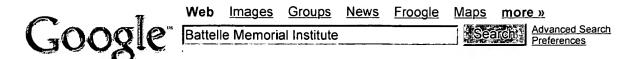
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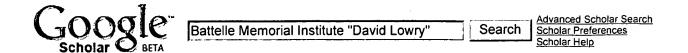
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